OIPE

```
                    RAW SEQUENCE LISTING              DATE: 05/16/2001
                    PATENT APPLICATION:  US/09/848,616   TIME: 13:46:54

                    ' Input Set : A:\seqlist 1700 0180002.txt
                      Output Set: N:\CRF3\05162001\I848616.raw

     4 <110> APPLICANT: Sebbel, Peter
     5         Dunant, Nicolas
     6         Bachmann, Martin
     7         Tissot, Alain
     8         Lechner, Franziska
    10 <120> TITLE OF INVENTION: Molecular Antigen Array
    13 <130> FILE REFERENCE: 1700.0180002
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/848,616
C--> 16 <141> CURRENT FILING DATE: 2001-05-04
    18 <160> NUMBER OF SEQ ID NOS: 186
    20 <170> SOFTWARE: PatentIn Ver. 2.1
    22 <210> SEQ ID NO: 1
    23 <211> LENGTH: 41
    24 <212> TYPE: DNA
    25 <213> ORGANISM: Artificial Sequence
    27 <220> FEATURE:
    28 <223> OTHER INFORMATION: Primer
    30 <400> SEQUENCE: 1
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    34 <210> SEQ ID NO: 2
    35 <211> LENGTH: 44
    36 <212> TYPE: DNA
    37 <213> ORGANISM: Artificial Sequence
    39 <220> FEATURE:
    40 <223> OTHER INFORMATION: Primer
    42 <400> SEQUENCE: 2
    43 cggtggttac ctgctgcacg cgttgcttaa gcgacatgta gcgg            44
    46 <210> SEQ ID NO: 3
    47 <211> LENGTH: 20
    48 <212> TYPE: DNA
    49 <213> ORGANISM: Artificial Sequence
    51 <220> FEATURE:
    52 <223> OTHER INFORMATION: Primer
    54 <400> SEQUENCE: 3
    55 ccatgaggcc tacgataccc                                       20
    58 <210> SEQ ID NO: 4
    59 <211> LENGTH: 25
    60 <212> TYPE: DNA
    61 <213> ORGANISM: Artificial Sequence
    63 <220> FEATURE:
    64 <223> OTHER INFORMATION: Primer
    66 <400> SEQUENCE: 4
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    70 <210> SEQ ID NO: 5
    71 <211> LENGTH: 47
    72 <212> TYPE: DNA
    73 <213> ORGANISM: Artificial Sequence
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 75 <220> FEATURE:
 76 <223> OTHER INFORMATION: Primer
 78 <400> SEQUENCE: 5
 79 ccttctttaa cggtggttac ctgctggcaa ccaacgtggt tcatgac              47
 82 <210> SEQ ID NO: 6
 83 <211> LENGTH: 40
 84 <212> TYPE: DNA
 85 <213> ORGANISM: Artificial Sequence
 87 <220> FEATURE:
 88 <223> OTHER INFORMATION: Primer
 90 <400> SEQUENCE: 6
 91 aagcatgctg cacgcgtgtg cggtggtcgg atcgcccggc                      40
 94 <210> SEQ ID NO: 7
 95 <211> LENGTH: 90
 96 <212> TYPE: DNA
 97 <213> ORGANISM: Artificial Sequence
 99 <220> FEATURE:
100 <223> OTHER INFORMATION: Primer
102 <400> SEQUENCE: 7
103 gggtctagat tcccaaccat tcccttatcc aggctttttg acaacgctat gctccgcgcc 60
104 catcgtctgc accagctggc ctttgacacc                                 90
107 <210> SEQ ID NO: 8
108 <211> LENGTH: 108
109 <212> TYPE: DNA
110 <213> ORGANISM: Artificial Sequence
112 <220> FEATURE:
113 <223> OTHER INFORMATION: Primer
115 <400> SEQUENCE: 8
116 gggtctagaa ggaggtaaaa aacgatgaaa aagacagcta tcgcgattgc agtggcactg 60
117 gctggtttcg ctaccgtagc gcaggccttc ccaaccattc ccttatcc             108
120 <210> SEQ ID NO: 9
121 <211> LENGTH: 31
122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: Primer
128 <400> SEQUENCE: 9
129 cccgaattcc tagaagccac agctgccctc c                               31
132 <210> SEQ ID NO: 10
133 <211> LENGTH: 24
134 <212> TYPE: DNA
135 <213> ORGANISM: Artificial Sequence
137 <220> FEATURE:
138 <223> OTHER INFORMATION: Primer
140 <400> SEQUENCE: 10
141 cctgcggtgg tctgaccgac accc                                       24
144 <210> SEQ ID NO: 11
145 <211> LENGTH: 41
146 <212> TYPE: DNA
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147 <213> ORGANISM: Artificial Sequence
149 <220> FEATURE:
150 <223> OTHER INFORMATION: Primer
152 <400> SEQUENCE: 11
153 ccgcggaaga gccaccgcaa ccaccgtgtg ccgccaggat g                    41
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157 <211> LENGTH: 33
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: Primer
164 <400> SEQUENCE: 12
165 ctatcatcta gaatgaatag aggattcttt aac                             33
168 <210> SEQ ID NO: 13
169 <211> LENGTH: 15
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Modified ribosome
175         binding site
177 <400> SEQUENCE: 13
178 aggaggtaaa aaacg                                                 15
181 <210> SEQ ID NO: 14
182 <211> LENGTH: 21
183 <212> TYPE: PRT
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: signal peptide
189 <400> SEQUENCE: 14
190 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
191  1               5                  10                  15
193 Thr Val Ala Gln Ala
194             20
197 <210> SEQ ID NO: 15
198 <211> LENGTH: 46
199 <212> TYPE: PRT
200 <213> ORGANISM: Artificial Sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: modified Fos
204         construct
206 <400> SEQUENCE: 15
207 Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu
208  1               5                  10                  15
210 Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu
211             20                  25                  30
213 Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys
214             35                  40                  45
217 <210> SEQ ID NO: 16
218 <211> LENGTH: 6
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```
219 <212> TYPE: PRT
220 <213> ORGANISM: Artificial Sequence
222 <220> FEATURE:
223 <223> OTHER INFORMATION: peptide linker
225 <400> SEQUENCE: 16
226 Ala Ala Ala Ser Gly Gly
227   1           5
230 <210> SEQ ID NO: 17
231 <211> LENGTH: 6
232 <212> TYPE: PRT
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: peptide linker
238 <400> SEQUENCE: 17
239 Gly Gly Ser Ala Ala Ala
240   1           5
243 <210> SEQ ID NO: 18
244 <211> LENGTH: 256
245 <212> TYPE: DNA
246 <213> ORGANISM: Artificial Sequence
248 <220> FEATURE:
249 <223> OTHER INFORMATION: Fos fusion construct
251 <400> SEQUENCE: 18
252 gaattcagga ggtaaaaaac gatgaaaaag acagctatcg cgattgcagt ggcactggct 60
253 ggtttcgcta ccgtagcgca ggcctgggtg ggggcggccg cttctggtgg ttgcggtggt 120
254 ctgaccgaca ccctgcaggc ggaaaccgac caggtggaag acgaaaaatc cgcgctgcaa 180
255 accgaaatcg cgaacctgct gaaagaaaaa gaaaagctgg agttcatcct ggcggcacac 240
256                                          ggtggttgct aagctt
```

⟵ move to left

```
259 <210> SEQ ID NO: 19
260 <211> LENGTH: 52
261 <212> TYPE: PRT
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Fos fusion construct
267 <400> SEQUENCE: 19
268 Ala Ala Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala
269               5                   10                  15
271 Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile
272               20                  25                  30
274 Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala
275               35                  40                  45
277 His Gly Gly Cys
278       50
282 <210> SEQ ID NO: 20
283 <211> LENGTH: 261
284 <212> TYPE: DNA
285 <213> ORGANISM: Artificial Sequence
287 <220> FEATURE:
288 <223> OTHER INFORMATION: Fos fusion
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Input Set : A:\seqlist 1700 0180002.txt
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289        construct
291 <220> FEATURE:
292 <221> NAME/KEY: CDS
293 <222> LOCATION: (22)..(240)
295 <400> SEQUENCE: 20
296 gaattcagga ggtaaaaaac g atg aaa aag aca gct atc gcg att gca gtg   51
297                         Met Lys Lys Thr Ala Ile Ala Ile Ala Val
298                          1               5                  10
300 gca ctg gct ggt ttc gct acc gta gcg cag gcc tgc ggt ggt ctg acc   99
301 Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Cys Gly Gly Leu Thr
302              15                  20                  25
304 gac acc ctg cag gcg gaa acc gac cag gtg gaa gac gaa aaa tcc gcg  147
305 Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala
306              30                  35                  40
308 ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa gaa aag ctg gag  195
309 Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu
310              45                  50                  55
312 ttc atc ctg gcg gca cac ggt ggt tgc ggt ggt tct gcg gcc gct      240
313 Phe Ile Leu Ala Ala His Gly Gly Cys Gly Gly Ser Ala Ala Ala
314      60                  65                  70
316 gggtgtgggg atatcaagct t                                           261
319 <210> SEQ ID NO: 21
320 <211> LENGTH: 73
321 <212> TYPE: PRT
322 <213> ORGANISM: Artificial Sequence
324 <220> FEATURE:
325 <223> OTHER INFORMATION: Fos fusion
326        construct
328 <400> SEQUENCE: 21
329 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
330   1               5                  10                  15
332 Thr Val Ala Gln Ala Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu
333              20                  25                  30
335 Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala
336              35                  40                  45
338 Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His
339      50                  55                  60
341 Gly Gly Cys Gly Gly Ser Ala Ala Ala
342   65                  70
346 <210> SEQ ID NO: 22
347 <211> LENGTH: 196
348 <212> TYPE: DNA
349 <213> ORGANISM: Artificial Sequence
351 <220> FEATURE:
352 <223> OTHER INFORMATION: Fos fusion
353        construct
355 <220> FEATURE:
356 <221> NAME/KEY: CDS
357 <222> LOCATION: (34)..(189)
```

Please Note:
Use f n and/ r Xaa have been detect d in the Sequence Listing. Please review the Sequence Listing to ensure that a c rresponding explanati n is presented in the <220> to <223> fields f each sequence which presents at least ne n r Xaa.

VERIFICATION SUMMARY   DATE: 05/16/2001
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    Input Set : A:\seqlist 1700 0180002.txt
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L:15 M:270 C: Current Application Number differs, Replaced Application Number
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:381 M:283 W: Missing Blank Line separator, <220> field identifier
L:2378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:111